

## SEQUENCE LISTING

<110> Schimmel, Paul  
Wakasugi, Keisuke

<120> Human Aminoacyl-tRNA Synthetase Polypeptides Useful For  
The Regulation of Angiogenesis

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<170> PatentIn Ver. 2.0

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<223> Description of Artificial Sequence: human  
full-length TyrRS in pET20B

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<223> Description of Artificial Sequence: human  
full-length TyrRS in pET20B

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<223> Description of Artificial Sequence: human mini  
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acgttttgca	gcagcagtcg	cttcacgttc	gctcgcgtat	cggtgattca	ttctgctaac	3240
cagtaaggca	accccgccag	cctagccggg	tcctcaacga	caggagcacg	atcatgcgca	3300
cccgtggcca	ggaccaaacg	ctgcccgaga	tctcgatccc	gcgaaattaa	tacgactcac	3360
tatagggaga	ccacaacggt	ttccctctag	aaataatttt	gtttaacttt	aagaaggaga	3420
tatacat	atg ggg gac gct ccc agc cct gaa gag aaa ctg cac ctt atc	3469				
	Met Gly Asp Ala Pro Ser Pro Glu Glu Lys Leu His Leu Ile					
	1                        5                        10					
acc cgg aac ctg cag gag gtt ctg ggg gaa gag aag ctg aag gag ata	3517					
Thr Arg Asn Leu Gln Glu Val Leu Gly Glu Glu Lys Leu Lys Glu Ile						
15                        20                        25                        30						
ctg aag gag cgg gaa ctt aaa att tac tgg gga acg gca acc acg ggc	3565					
Leu Lys Glu Arg Glu Leu Lys Ile Tyr Trp Gly Thr Ala Thr Thr Gly						
35                        40                        45						
aaa cca cat gtg gct tac ttt gtg ccc atg tca aag att gca gac ttc	3613					
Lys Pro His Val Ala Tyr Phe Val Pro Met Ser Lys Ile Ala Asp Phe						
50                        55                        60						
tta aag gca ggg tgt gag gta aca att ctg ttt gcg gac ctc cac gca	3661					
Leu Lys Ala Gly Cys Glu Val Thr Ile Leu Phe Ala Asp Leu His Ala						
65                        70                        75						
tac ctg gat aac atg aaa gcc cca tgg gaa ctt cta gaa ctc cga gtc	3709					
Tyr Leu Asp Asn Met Lys Ala Pro Trp Glu Leu Leu Glu Leu Arg Val						
80                        85                        90						
agt tac tat gag aat gtg atc aaa gca atg ctg gag agc att ggt gtg	3757					
Ser Tyr Tyr Glu Asn Val Ile Lys Ala Met Leu Glu Ser Ile Gly Val						
95                        100                        105                        110						

ccc ttg gag aag ctc aag ttc atc aaa ggc act gat tac cag ctc agc	3805
Pro Leu Glu Lys Leu Lys Phe Ile Lys Gly Thr Asp Tyr Gln Leu Ser	
115 120 125	
aaa gag tac aca cta gat gtg tac aga ctc tcc tcc gtg gtc aca cag	3853
Lys Glu Tyr Thr Leu Asp Val Tyr Arg Leu Ser Ser Val Val Thr Gln	
130 135 140	
cac gat tcc aag aag gct gga gct gag gtg gta aag cag gtg gag cac	3901
His Asp Ser Lys Lys Ala Gly Ala Glu Val Val Lys Gln Val Glu His	
145 150 155	
cct ttg ctg agt ggc ctc tta tac ccc gga ctg cag gct ttg gat gaa	3949
Pro Leu Leu Ser Gly Leu Leu Tyr Pro Gly Leu Gln Ala Leu Asp Glu	
160 165 170	
gag tat tta aaa gta gat gcc caa ttt gga ggc att gat cag aga aag	3997
Glu Tyr Leu Lys Val Asp Ala Gln Phe Gly Gly Ile Asp Gln Arg Lys	
175 180 185 190	
att ttc acc ttt gca gag aag tac ctc cct gca ctt ggc tat tca aaa	4045
Ile Phe Thr Phe Ala Glu Lys Tyr Leu Pro Ala Leu Gly Tyr Ser Lys	
195 200 205	
cgg gtc cat ctg atg aat cct atg gtt cca gga tta aca ggc agc aaa	4093
Arg Val His Leu Met Asn Pro Met Val Pro Gly Leu Thr Gly Ser Lys	
210 215 220	
atg agc tct tca gaa gag gag tcc aag att gat ctc ctt gat cgg aag	4141
Met Ser Ser Ser Glu Glu Glu Ser Lys Ile Asp Leu Leu Asp Arg Lys	
225 230 235	
gag gat gtg aag aaa aaa ctg aag aag gcc ttc tgt gag cca gga aat	4189
Glu Asp Val Lys Lys Lys Leu Lys Lys Ala Phe Cys Glu Pro Gly Asn	
240 245 250	
gtg gag aac aat ggg gtt ctg tcc ttc atc aag cat gtc ctt ttt ccc	4237
Val Glu Asn Asn Gly Val Leu Ser Phe Ile Lys His Val Leu Phe Pro	
255 260 265 270	
ctt aag tcc gag ttt gtg atc cta cga gat gag aaa tgg ggt gga aac	4285
Leu Lys Ser Glu Phe Val Ile Leu Arg Asp Glu Lys Trp Gly Gly Asn	
275 280 285	
aaa acc tac aca gct tac gtg gac ctg gaa aag gac ttt gct gct gag	4333
Lys Thr Tyr Thr Ala Tyr Val Asp Leu Glu Lys Asp Phe Ala Ala Glu	
290 295 300	
gtt gta cat cct gga gac ctg aag aat tct gtt gaa gtc gca ctg aac	4381
Val Val His Pro Gly Asp Leu Lys Asn Ser Val Glu Val Ala Leu Asn	
305 310 315	
aag ttg ctg gat cca atc cgg gaa aag ttt aat acc cct gcc ctg aaa	4429
Lys Leu Leu Asp Pro Ile Arg Glu Lys Phe Asn Thr Pro Ala Leu Lys	
320 325 330	
aaa ctg gcc agc gct gcc tac cca gat ccc tca aag cag aag cca atg	4477
Lys Leu Ala Ser Ala Ala Tyr Pro Asp Pro Ser Lys Gln Lys Pro Met	
335 340 345 350	

gcc aaa ggc cct gcc aag aat tca gaa cca gag gag gtc atc ctc gag 4525  
 Ala Lys Gly Pro Ala Lys Asn Ser Glu Pro Glu Glu Val Ile Leu Glu  
                   355                                  360                                  365

cac cac cac cac cac cac tgagatccgg ctgctaacaa agcccgaaag 4573  
 His His His His His His  
                   370

gaagctgagt tggctgctgc caccgctgag caataactag cataaccctt tggggcctct 4633

aaacgggtct tgaggggttt tttgctgaaa ggaggaacta tatccggat 4682

<210> 4

<211> 372

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: human mini  
 TyrRS in pET20B

<400> 4

Met Gly Asp Ala Pro Ser Pro Glu Glu Lys Leu His Leu Ile Thr Arg  
   1                                  5                                  10                                  15

Asn Leu Gln Glu Val Leu Gly Glu Glu Lys Leu Lys Glu Ile Leu Lys  
                   20                                  25                                  30

Glu Arg Glu Leu Lys Ile Tyr Trp Gly Thr Ala Thr Thr Gly Lys Pro  
                   35                                  40                                  45

His Val Ala Tyr Phe Val Pro Met Ser Lys Ile Ala Asp Phe Leu Lys  
                   50                                  55                                  60

Ala Gly Cys Glu Val Thr Ile Leu Phe Ala Asp Leu His Ala Tyr Leu  
                   65                                  70                                  75                                  80

Asp Asn Met Lys Ala Pro Trp Glu Leu Leu Glu Leu Arg Val Ser Tyr  
                                   85                                  90                                  95

Tyr Glu Asn Val Ile Lys Ala Met Leu Glu Ser Ile Gly Val Pro Leu  
                   100                                  105                                  110

Glu Lys Leu Lys Phe Ile Lys Gly Thr Asp Tyr Gln Leu Ser Lys Glu  
                   115                                  120                                  125

Tyr Thr Leu Asp Val Tyr Arg Leu Ser Ser Val Val Thr Gln His Asp  
                   130                                  135                                  140

Ser Lys Lys Ala Gly Ala Glu Val Val Lys Gln Val Glu His Pro Leu  
                   145                                  150                                  155                                  160

Leu Ser Gly Leu Leu Tyr Pro Gly Leu Gln Ala Leu Asp Glu Glu Tyr  
                   165                                  170                                  175

Leu Lys Val Asp Ala Gln Phe Gly Gly Ile Asp Gln Arg Lys Ile Phe  
                   180                                  185                                  190

Thr Phe Ala Glu Lys Tyr Leu Pro Ala Leu Gly Tyr Ser Lys Arg Val  
                   195                                  200                                  205

His Leu Met Asn Pro Met Val Pro Gly Leu Thr Gly Ser Lys Met Ser  
 210 215 220

Ser Ser Glu Glu Glu Ser Lys Ile Asp Leu Leu Asp Arg Lys Glu Asp  
 225 230 235 240

Val Lys Lys Lys Leu Lys Lys Ala Phe Cys Glu Pro Gly Asn Val Glu  
 245 250 255

Asn Asn Gly Val Leu Ser Phe Ile Lys His Val Leu Phe Pro Leu Lys  
 260 265 270

Ser Glu Phe Val Ile Leu Arg Asp Glu Lys Trp Gly Gly Asn Lys Thr  
 275 280 285

Tyr Thr Ala Tyr Val Asp Leu Glu Lys Asp Phe Ala Ala Glu Val Val  
 290 295 300

His Pro Gly Asp Leu Lys Asn Ser Val Glu Val Ala Leu Asn Lys Leu  
 305 310 315 320

Leu Asp Pro Ile Arg Glu Lys Phe Asn Thr Pro Ala Leu Lys Lys Leu  
 325 330 335

Ala Ser Ala Ala Tyr Pro Asp Pro Ser Lys Gln Lys Pro Met Ala Lys  
 340 345 350

Gly Pro Ala Lys Asn Ser Glu Pro Glu Glu Val Ile Leu Glu His His  
 355 360 365

His His His His  
 370

<210> 5  
 <211> 4100  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (3428)..(3961)

<220>  
 <223> Description of Artificial Sequence: human TyrRS  
 carboxyl-terminal domain in pET20B

<400> 5  
 tggcgaatgg gacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg tggttacgcg 60  
 cagcgtgacc gctacacttg ccagcgcacct agcgcgccgt cctttcgttt tcttcccttc 120  
 ctttctcgcc acgttcgccg gctttccccg tcaagctcta aatcgggggc tccctttagg 180  
 gttccgattt agtgctttac ggcacctga ccccaaaaaa cttgattagg gtgatggttc 240  
 acgtagtggg ccacgcacct gatagacggt ttttcgccct ttgacgttgg agtccacgtt 300  
 ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggtctattc 360  
 ttttgattta taagggattt tgccgatttc ggcctattgg ttaaaaaatg agctgattta 420

acaaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt 480  
 tcgggggaaat gtgcgcggaa cccctatttg tttatttttc taaatacatt caaatatgta 540  
 tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa ggaagagtat 600  
 gagtattcaa catttccgtg tcgcccttat tccctttttt gcggcatttt gccttctgt 660  
 ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg 720  
 agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt ttgcgccga 780  
 agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg tattatcccg 840  
 tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga atgacttggt 900  
 tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa gagaattatg 960  
 cagtgtgcc ataaccatga gtgataacac tgcggccaac ttacttctga caacgatcgg 1020  
 aggaccgaag gagctaaccg cttttttgca caacatgggg gatcatgtaa ctgccttga 1080  
 tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca ccacgatgcc 1140  
 tgcagcaatg gcaacaacgt tgcgcaaaact attaactggc gaactactta ctctagcttc 1200  
 ccggcaacaa ttaatagact ggatggaggc ggataaagtt gcaggaccac ttctgcgctc 1260  
 ggcccttccg gctggctggt ttattgctga taaatctgga gccggtgagc gtgggtctcg 1320  
 cggatatcatt gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac 1380  
 gacggggagt caggcaacta tggatgaacg aaatagacag atcgtgaga taggtgcctc 1440  
 actgattaag cattggtaac tgtcagacca agtttactca tatatacttt agattgattt 1500  
 aaaacttcat ttttaattta aaaggatcta ggtgaagatc ctttttgata atctcatgac 1560  
 caaaatccct taacgtgagt tttcgttcca ctgagcgtca gaccccgtag aaaagatcaa 1620  
 aggatcttct tgagatcctt tttttctgcg cgtaatctgc tgcttgcaaa caaaaaaacc 1680  
 accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt ttccgaaggt 1740  
 aactggcttc agcagagcgc agataccaaa tactgtcctt ctagtgtagc cgtagttagg 1800  
 ccaccacttc aagaactctg tagcaccgcc tacatactc gctctgctaa tcctgttacc 1860  
 agtggctgct gccagtggcg ataagtcgtg tcttaccggg ttggactcaa gacgatagtt 1920  
 accggataag gcgcagcggc cgggctgaac ggggggttcg tgcacacagc ccagcttga 1980  
 gcgaacgacc tacaccgaac tgagatacct acagcgtgag ctatgagaaa gcgccacgct 2040  
 tcccgaaggg agaaaggcgg acaggtatcc ggtaagcggc agggtcggaa caggagagcg 2100  
 cagcaggag cttccagggg gaaacgcctg gtatctttat agtcctgtcg ggtttcgcc 2160  
 cctctgactt gagcgtcgat ttttgatg ctgcgcagg ggcggagcc tatggaaaaa 2220  
 cgccagcaac gcggcctttt tacggttctt ggccttttgc tggccttttg ctcacatggt 2280

ctttcctgcg ttatccctg attctgtgga taaccgtatt accgcctttg agtgagctga 2340  
 taccgctcgc cgcagccgaa cgaccgagcg cagcgagtca gtgagcgagg aagcgggaaga 2400  
 gcgcctgatg cggatattttc tccttacgca tctgtgcggt atttcacacc gcatatatgg 2460  
 tgcactctca gtacaatctg ctctgatgcc gcatagttaa gccagtatac actccgctat 2520  
 cgctacgtga ctgggtcatg gctgcgcccc gacacccgcc aacacccgct gacgcgccct 2580  
 gacgggcttg tctgctcccg gcatccgctt acagacaagc tgtgaccgtc tccgggagct 2640  
 gcatgtgtca gaggttttca ccgtcatcac cgaaacgcgc gaggcagctg cggtaaagct 2700  
 catcagcgtg gtcgtgaagc gattcacaga tgtctgcctg ttcacccgcg tccagctcgt 2760  
 tgagtttctc cagaagcgtt aatgtctggc ttctgataaa gcggggccatg ttaagggcgg 2820  
 ttttttctcg tttggctact gatgcctcgg tgtaaggggg atttctgttc atgggggtaa 2880  
 tgataccgat gaaacgagag aggatgctca cgatacgggt tactgatgat gaacatgccc 2940  
 gggttactgga acgttgtgag ggtaaacaac tggcgggtatg gatgcggcgg gaccagagaa 3000  
 aaatcactca gggtaaatgc cagcgcttcg ttaatacaga tgtaggtggt ccacagggta 3060  
 gccagcagca tcctgcgatg cagatccgga acataatggt gcagggcgct gacttccgcg 3120  
 tttccagact ttacgaaaca cggaaaccga agaccattca tgttggttgc caggtcgcag 3180  
 acgttttgca gcagcagtcg cttcacgttc gtcgcgctat cggtgattca ttctgctaac 3240  
 cagtaaggca accccgccag cctagccggg tcctcaacga caggagcacg atcatgcgca 3300  
 cccgtggcca ggacccaacg ctgcccgaga tctcgatccc gcgaaattaa tacgactcac 3360  
 tatagggaga ccacaacggt ttccctctag aaataatttt gtttaacttt aagaaggaga 3420  
 tatacat atg cca gag gag gtc atc cca tcc cgg ctg gat atc cgt gtg 3469  
 Met Pro Glu Glu Val Ile Pro Ser Arg Leu Asp Ile Arg Val  
 1 5 10  
 ggg aaa atc atc act gtg gag aag cac cca gat gca gac agc ctg tat 3517  
 Gly Lys Ile Ile Thr Val Glu Lys His Pro Asp Ala Asp Ser Leu Tyr  
 15 20 25 30  
 gta gag aag att gac gtg ggg gaa gct gaa cca cgg act gtg gtg agc 3565  
 Val Glu Lys Ile Asp Val Gly Glu Ala Glu Pro Arg Thr Val Val Ser  
 35 40 45  
 ggc ctg gta cag ttc gtg ccc aag gag gaa ctg cag gac agg ctg gta 3613  
 Gly Leu Val Gln Phe Val Pro Lys Glu Glu Leu Gln Asp Arg Leu Val  
 50 55 60  
 gtg gtg ctg tgc aac ctg aaa ccc cag aag atg aga gga gtc gag tcc 3661  
 Val Val Leu Cys Asn Leu Lys Pro Gln Lys Met Arg Gly Val Glu Ser  
 65 70 75  
 caa ggc atg ctt ctg tgt gct tct ata gaa ggg ata aac cgc cag gtt 3709  
 Gln Gly Met Leu Leu Cys Ala Ser Ile Glu Gly Ile Asn Arg Gln Val  
 80 85 90

gaa cct ctg gac cct ccg gca ggc tct gct cct ggt gag cac gtg ttt 3757  
 Glu Pro Leu Asp Pro Pro Ala Gly Ser Ala Pro Gly Glu His Val Phe  
 95 100 105 110

gtg aag ggc tat gaa aag ggc caa cca gat gag gag ctc aag ccc aag 3805  
 Val Lys Gly Tyr Glu Lys Gly Gln Pro Asp Glu Glu Leu Lys Pro Lys  
 115 120 125

aag aaa gtc ttc gag aag ttg cag gct gac ttc aaa att tct gag gag 3853  
 Lys Lys Val Phe Glu Lys Leu Gln Ala Asp Phe Lys Ile Ser Glu Glu  
 130 135 140

tgc atc gca cag tgg aag caa acc aac ttc atg acc aag ctg ggc tcc 3901  
 Cys Ile Ala Gln Trp Lys Gln Thr Asn Phe Met Thr Lys Leu Gly Ser  
 145 150 155

att tcc tgt aaa tcg ctg aaa ggg ggg aac att agc ctc gag cac cac 3949  
 Ile Ser Cys Lys Ser Leu Lys Gly Gly Asn Ile Ser Leu Glu His His  
 160 165 170

cac cac cac cac tgagatccgg ctgctaacaa agcccgaag gaagctgagt 4001  
 His His His His  
 175

tggctgctgc caccgctgag caataactag cataaccct tggggcctct aaacgggtct 4061

tgagggggttt tttgctgaaa ggaggaacta tatccggat 4100

<210> 6

<211> 178

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: human TyrRS  
 carboxyl-terminal domain in pET20B

<400> 6

Met Pro Glu Glu Val Ile Pro Ser Arg Leu Asp Ile Arg Val Gly Lys  
 1 5 10 15

Ile Ile Thr Val Glu Lys His Pro Asp Ala Asp Ser Leu Tyr Val Glu  
 20 25 30

Lys Ile Asp Val Gly Glu Ala Glu Pro Arg Thr Val Val Ser Gly Leu  
 35 40 45

Val Gln Phe Val Pro Lys Glu Glu Leu Gln Asp Arg Leu Val Val Val  
 50 55 60

Leu Cys Asn Leu Lys Pro Gln Lys Met Arg Gly Val Glu Ser Gln Gly  
 65 70 75 80

Met Leu Leu Cys Ala Ser Ile Glu Gly Ile Asn Arg Gln Val Glu Pro  
 85 90 95

Leu Asp Pro Pro Ala Gly Ser Ala Pro Gly Glu His Val Phe Val Lys  
 100 105 110

Gly Tyr Glu Lys Gly Gln Pro Asp Glu Glu Leu Lys Pro Lys Lys Lys  
 115 120 125

Val Phe Glu Lys Leu Gln Ala Asp Phe Lys Ile Ser Glu Glu Cys Ile  
 130 135 140

Ala Gln Trp Lys Gln Thr Asn Phe Met Thr Lys Leu Gly Ser Ile Ser  
 145 150 155 160

Cys Lys Ser Leu Lys Gly Gly Asn Ile Ser Leu Glu His His His His  
 165 170 175

His His

<210> 7  
 <211> 4682  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (3428)..(4543)

<220>  
 <223> Description of Artificial Sequence: human mini  
 TyrRS mutant in pET20B

<400> 7  
 tggcgaatgg gacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg tggttacgcg 60  
 cagcgtgacc gctacacttg ccagcgccct agcgcccgct ctttctgctt tcttcccttc 120  
 ctttctcgcc acgttcgccg gctttccccg tcaagctcta aatcgggggc tcccttttagg 180  
 gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc 240  
 acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacggt 300  
 ctttaatatg ggactcttgt tccaaactgg aacaacactc aaccctatct cgggtctattc 360  
 ttttgattta taagggaatt tgccgatttc ggcctatttg ttaaaaaatg agctgattta 420  
 acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt 480  
 tcggggaaat gtgcgcggaa cccctatttg tttatttttc taaatacatt caaatatgta 540  
 tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa ggaagagtat 600  
 gagtattcaa catttccgtg tcgccttat tccctttttt gcggcatttt gccttcctgt 660  
 ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg 720  
 agtgggttac atcgaactgg atctcaacag cggtgaagatc cttgagagtt ttcgccccga 780  
 agaacgtttt ccaatgatga gcactttttaa agttctgcta tgtggcgcgg tattatcccg 840  
 tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga atgacttggt 900  
 tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa gagaattatg 960  
 cagtgtgcc ataaccatga gtgataaacac tgcgggccaac ttacttctga caacgatcgg 1020





tgataaccgat	gaaacgagag	aggatgctca	cgatacgggt	tactgatgat	gaacatgccc	2940
ggttactgga	acgttgtgag	ggtaaacaac	tggcggtatg	gatgcggcgg	gaccagagaa	3000
aaatcactca	gggtcaatgc	cagcgcttcg	ttaatacaga	tgtaggtggt	ccacagggta	3060
gccagcagca	tcttgcgatg	cagatccgga	acataatggt	gcagggcgct	gacttccgcg	3120
tttccagact	ttacgaaaca	cggaaaccga	agaccattca	tgttggtgct	caggtcgcag	3180
acgttttgca	gcagcagtcg	cttcacgttc	gctcgcgtat	cggtgattca	ttctgctaac	3240
cagtaaggca	accccgccag	cctagccggg	tcctcaacga	caggagcacg	atcatgcgca	3300
cccgtggcca	ggacccaacg	ctgcccgaga	tctcgatccc	gcgaaattaa	tacgactcac	3360
tatagggaga	ccacaacggt	ttccctctag	aaataatttt	gtttaacttt	aagaaggaga	3420
tatacat	atg ggg gac gct ccc agc cct gaa gag aaa ctg cac ctt atc	3469				
	Met Gly Asp Ala Pro Ser Pro Glu Glu Lys Leu His Leu Ile					
	1 5 10					
acc cgg aac ctg cag gag gtt ctg ggg gaa gag aag ctg aag gag ata	3517					
Thr Arg Asn Leu Gln Glu Val Leu Gly Glu Glu Lys Leu Lys Glu Ile						
15 20 25 30						
ctg aag gag cgg gaa ctt aaa att tac tgg gga acg gca acc acg ggc	3565					
Leu Lys Glu Arg Glu Leu Lys Ile Tyr Trp Gly Thr Ala Thr Thr Gly						
35 40 45						
aaa cca cat gtg gct tac ttt gtg ccc atg tca aag att gca gac ttc	3613					
Lys Pro His Val Ala Tyr Phe Val Pro Met Ser Lys Ile Ala Asp Phe						
50 55 60						
tta aag gca ggg tgt gag gta aca att ctg ttt gcg gac ctc cac gca	3661					
Leu Lys Ala Gly Cys Glu Val Thr Ile Leu Phe Ala Asp Leu His Ala						
65 70 75						
tac ctg gat aac atg aaa gcc cca tgg gaa ctt cta gaa ctg cag gtc	3709					
Tyr Leu Asp Asn Met Lys Ala Pro Trp Glu Leu Leu Glu Leu Gln Val						
80 85 90						
agt tac tat gag aat gtg atc aaa gca atg ctg gag agc att ggt gtg	3757					
Ser Tyr Tyr Glu Asn Val Ile Lys Ala Met Leu Glu Ser Ile Gly Val						
95 100 105 110						
ccc ttg gag aag ctc aag ttc atc aaa ggc act gat tac cag ctc agc	3805					
Pro Leu Glu Lys Leu Lys Phe Ile Lys Gly Thr Asp Tyr Gln Leu Ser						
115 120 125						
aaa gag tac aca cta gat gtg tac aga ctc tcc tcc gtg gtc aca cag	3853					
Lys Glu Tyr Thr Leu Asp Val Tyr Arg Leu Ser Ser Val Val Thr Gln						
130 135 140						
cac gat tcc aag aag gct gga gct gag gtg gta aag cag gtg gag cac	3901					
His Asp Ser Lys Lys Ala Gly Ala Glu Val Val Lys Gln Val Glu His						
145 150 155						
cct ttg ctg agt ggc ctc tta tac ccc gga ctg cag gct ttg gat gaa	3949					
Pro Leu Leu Ser Gly Leu Leu Tyr Pro Gly Leu Gln Ala Leu Asp Glu						
160 165 170						

gag tat tta aaa gta gat gcc caa ttt gga ggc att gat cag aga aag 3997  
 Glu Tyr Leu Lys Val Asp Ala Gln Phe Gly Gly Ile Asp Gln Arg Lys  
 175 180 185 190

att ttc acc ttt gca gag aag tac ctc cct gca ctt ggc tat tca aaa 4045  
 Ile Phe Thr Phe Ala Glu Lys Tyr Leu Pro Ala Leu Gly Tyr Ser Lys  
 195 200 205

cgg gtc cat ctg atg aat cct atg gtt cca gga tta aca ggc agc aaa 4093  
 Arg Val His Leu Met Asn Pro Met Val Pro Gly Leu Thr Gly Ser Lys  
 210 215 220

atg agc tct tca gaa gag gag tcc aag att gat ctc ctt gat cgg aag 4141  
 Met Ser Ser Ser Glu Glu Glu Ser Lys Ile Asp Leu Leu Asp Arg Lys  
 225 230 235

gag gat gtg aag aaa aaa ctg aag aag gcc ttc tgt gag cca gga aat 4189  
 Glu Asp Val Lys Lys Lys Leu Lys Lys Ala Phe Cys Glu Pro Gly Asn  
 240 245 250

gtg gag aac aat ggg gtt ctg tcc ttc atc aag cat gtc ctt ttt ccc 4237  
 Val Glu Asn Asn Gly Val Leu Ser Phe Ile Lys His Val Leu Phe Pro  
 255 260 265 270

ctt aag tcc gag ttt gtg atc cta cga gat gag aaa tgg ggt gga aac 4285  
 Leu Lys Ser Glu Phe Val Ile Leu Arg Asp Glu Lys Trp Gly Gly Asn  
 275 280 285

aaa acc tac aca gct tac gtg gac ctg gaa aag gac ttt gct gct gag 4333  
 Lys Thr Tyr Thr Ala Tyr Val Asp Leu Glu Lys Asp Phe Ala Ala Glu  
 290 295 300

gtt gta cat cct gga gac ctg aag aat tct gtt gaa gtc gca ctg aac 4381  
 Val Val His Pro Gly Asp Leu Lys Asn Ser Val Glu Val Ala Leu Asn  
 305 310 315

aag ttg ctg gat cca atc cgg gaa aag ttt aat acc cct gcc ctg aaa 4429  
 Lys Leu Leu Asp Pro Ile Arg Glu Lys Phe Asn Thr Pro Ala Leu Lys  
 320 325 330

aaa ctg gcc agc gct gcc tac cca gat ccc tca aag cag aag cca atg 4477  
 Lys Leu Ala Ser Ala Ala Tyr Pro Asp Pro Ser Lys Gln Lys Pro Met  
 335 340 345 350

gcc aaa ggc cct gcc aag aat tca gaa cca gag gag gtc atc ctc gag 4525  
 Ala Lys Gly Pro Ala Lys Asn Ser Glu Pro Glu Glu Val Ile Leu Glu  
 355 360 365

cac cac cac cac cac cac tgagatccgg ctgctaacaa agcccgaag 4573  
 His His His His His His  
 370

gaagctgagt tggctgctgc caccgctgag caataactag cataaccctcct tggggcctct 4633

aaacgggtct tgaggggttt tttgctgaaa ggaggaacta tatccggat 4682

<210> 8  
 <211> 372  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: human mini  
 TyrRS mutant in pET20B

<400> 8  
 Met Gly Asp Ala Pro Ser Pro Glu Glu Lys Leu His Leu Ile Thr Arg  
 1 5 10 15  
 Asn Leu Gln Glu Val Leu Gly Glu Glu Lys Leu Lys Glu Ile Leu Lys  
 20 25 30  
 Glu Arg Glu Leu Lys Ile Tyr Trp Gly Thr Ala Thr Thr Gly Lys Pro  
 35 40 45  
 His Val Ala Tyr Phe Val Pro Met Ser Lys Ile Ala Asp Phe Leu Lys  
 50 55 60  
 Ala Gly Cys Glu Val Thr Ile Leu Phe Ala Asp Leu His Ala Tyr Leu  
 65 70 75 80  
 Asp Asn Met Lys Ala Pro Trp Glu Leu Leu Glu Leu Gln Val Ser Tyr  
 85 90 95  
 Tyr Glu Asn Val Ile Lys Ala Met Leu Glu Ser Ile Gly Val Pro Leu  
 100 105 110  
 Glu Lys Leu Lys Phe Ile Lys Gly Thr Asp Tyr Gln Leu Ser Lys Glu  
 115 120 125  
 Tyr Thr Leu Asp Val Tyr Arg Leu Ser Ser Val Val Thr Gln His Asp  
 130 135 140  
 Ser Lys Lys Ala Gly Ala Glu Val Val Lys Gln Val Glu His Pro Leu  
 145 150 155 160  
 Leu Ser Gly Leu Leu Tyr Pro Gly Leu Gln Ala Leu Asp Glu Glu Tyr  
 165 170 175  
 Leu Lys Val Asp Ala Gln Phe Gly Gly Ile Asp Gln Arg Lys Ile Phe  
 180 185 190  
 Thr Phe Ala Glu Lys Tyr Leu Pro Ala Leu Gly Tyr Ser Lys Arg Val  
 195 200 205  
 His Leu Met Asn Pro Met Val Pro Gly Leu Thr Gly Ser Lys Met Ser  
 210 215 220  
 Ser Ser Glu Glu Glu Ser Lys Ile Asp Leu Leu Asp Arg Lys Glu Asp  
 225 230 235 240  
 Val Lys Lys Lys Leu Lys Lys Ala Phe Cys Glu Pro Gly Asn Val Glu  
 245 250 255  
 Asn Asn Gly Val Leu Ser Phe Ile Lys His Val Leu Phe Pro Leu Lys  
 260 265 270

Ser Glu Phe Val Ile Leu Arg Asp Glu Lys Trp Gly Gly Asn Lys Thr  
 275 280 285  
 Tyr Thr Ala Tyr Val Asp Leu Glu Lys Asp Phe Ala Ala Glu Val Val  
 290 295 300  
 His Pro Gly Asp Leu Lys Asn Ser Val Glu Val Ala Leu Asn Lys Leu  
 305 310 315 320  
 Leu Asp Pro Ile Arg Glu Lys Phe Asn Thr Pro Ala Leu Lys Lys Leu  
 325 330 335  
 Ala Ser Ala Ala Tyr Pro Asp Pro Ser Lys Gln Lys Pro Met Ala Lys  
 340 345 350  
 Gly Pro Ala Lys Asn Ser Glu Pro Glu Glu Val Ile Leu Glu His His  
 355 360 365  
 His His His His  
 370

<210> 9  
 <211> 5018  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (3428)..(4879)

<220>  
 <223> Description of Artificial Sequence: human  
 full-length TrpRS in pET20B

<400> 9  
 tggcgaatgg gacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg tggttacgcg 60  
 cagcgtgacc gctacacttg ccagcgccct agcgcccgct cctttcgctt tcttcccttc 120  
 ctttctcgcc acgttcgcg gttttcccg tcaagctcta aatcgggggc tccctttagg 180  
 gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc 240  
 acgtagtggg ccatcgccct gatagaagg ttttcgccct ttgacgttgg agtccacgtt 300  
 ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggctctattc 360  
 ttttgattta taagggattt tgccgatttc ggccatttgg ttaaaaaatg agctgattta 420  
 acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt 480  
 tcggggaaat gtgcgcggaa cccctatttg tttatttttc taaatacatt caaatatgta 540  
 tccgctcatg agacaataac cctgataaat gttcaataa tattgaaaaa ggaagagtat 600  
 gagtattcaa catttccgtg tcgccttat tccctttttt gcggcatttt gccttctgt 660  
 ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg 720  
 agtgggttac atcgaactgg atctcaacag cggttaagatc cttgagagtt ttgcgcccca 780

agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcggt tattatcccg 840  
 tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga atgacttggt 900  
 tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa gagaattatg 960  
 cagtgtctgcc ataaccatga gtgataaacac tgcggccaac ttactttctga caacgatcgg 1020  
 aggaccgaag gagctaaccg cttttttgca caacatgggg gatcatgtaa ctgccttga 1080  
 tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca ccacgatgcc 1140  
 tgcagcaatg gcaacaacgt tgcgcaaact attaaactggc gaactactta ctctagcttc 1200  
 ccggcaacaa ttaatagact ggatggaggc ggataaagtt gcaggaccac ttctgcgctc 1260  
 ggcccttccg gctggctggt ttattgctga taaatctgga gccggtgagc gtgggtctcg 1320  
 cggatcatt gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac 1380  
 gacggggagt caggcaacta tggatgaacg aaatagacag atcgtctgaga taggtgcctc 1440  
 aetgattaag cattggtaac tgtcagacca agtttactca tatatacttt agattgattt 1500  
 aaaacttcat ttttaattta aaaggatcta ggtgaagatc ctttttgata atctcatgac 1560  
 caaaatccct taacgtgagt ttctgttoca ctgagcgtca gaccccgtag aaaagatcaa 1620  
 aggatcttct tgagatcctt tttttctgcg cgtaatctgc tgcttgcaaa caaaaaaacc 1680  
 accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt ttccgaaggt 1740  
 aactggcttc agcagagcgc agataccaaa tactgtcctt ctagtgtagc cgtagttagg 1800  
 ccaccacttc aagaactctg tagcaccgcc tacatacctc gctctgctaa tctgttacc 1860  
 agtggctgct gccagtggtg ataagtcgtg tcttaccggg ttggactcaa gacgatagtt 1920  
 accggataag gcgcagcgtt cgggctgaac ggggggttcg tgcacacagc ccagcttgga 1980  
 gcgaacgacc tacaccgaac tgagatacct acagcgtgag ctatgagaaa gcgccacgct 2040  
 tcccgaaggg agaaaggcgg acaggtatcc ggtaagcggc agggtcggaa caggagagcg 2100  
 cacgagggag cttccagggg gaaacgcctg gtatctttat agtcctgtcg ggtttcgcca 2160  
 cctctgactt gagcgtcgat ttttgtgatg ctgcgcaggg gggcgagacc tatggaaaaa 2220  
 cgcagcaac gcggcctttt tacggttctt ggcccttttg tggccttttg ctacatggt 2280  
 ctttctgog ttatccctg attctgtgga taaccgtatt accgcctttg agtgagctga 2340  
 tacgctcgc cgcagccgaa cgaccgagcg cagcgagtca gtgagcgagg aagcggaaga 2400  
 gcgcctgatg cggatatttc tcttacgca tctgtgcggt atttcacacc gcatatatgg 2460  
 tgcactctca gtacaatctg ctctgatgcc gcatagttaa gccagtatac actccgctat 2520  
 cgctacgtga ctgggtcatg gctgcgcccc gacaccgcgc aacaccgct gacgcgcct 2580  
 gacgggcttg tctgtcccg gcatccgctt acagacaagc tgtgaccgtc tccgggagct 2640

gc	atg	tgt	tca	gag	gtt	ttt	cac	ccg	tcat	cac	cga	aac	gcgc	gag	gcag	ctg	cg	gtaa	agct	2700	
cat	cag	cg	tg	gtg	aag	c	att	ca	gag	atc	gtt	ctg	ttc	atc	ccgc	tcc	ag	ctc	gt	2760	
tg	ag	ttt	ctc	cag	aag	cg	tt	aat	gt	ctg	gc	tt	ctg	ataa	gcg	ggcc	atg	tt	aag	ggcg	2820
tt	ttt	tc	ctg	tt	gg	tca	ct	gat	gc	ctc	cg	tg	ta	aag	ggg	g	att	tt	ctg	ttc	2880
tg	ata	ccg	at	gaa	ac	gag	ag	gat	gt	ctc	cg	ata	c	ggg	t	tact	gat	gat	gaa	cat	2940
gg	tact	gga	acg	tt	gt	gag	gg	taa	aca	aac	tgg	c	ggt	atg	gat	gc	ggc	gg	gacc	agag	3000
aa	at	cact	ca	ggg	tca	atg	cag	cg	ctt	cg	tt	ata	ta	ca	gag	gt	tt	cc	ac	agg	3060
gcc	ag	cag	ca	tc	tg	cg	atg	cag	at	cc	gg	a	ata	at	gg	t	gc	agg	gc	gct	3120
tt	tc	cag	act	tt	ac	gaa	aac	cg	gaa	acc	ga	ag	acc	att	ca	tg	tt	gt	t	gct	3180
ac	g	ttt	tg	ca	gc	ag	ctg	ctt	ca	cg	ttc	g	tc	gc	gt	at	cg	gt	gatt	ca	3240
cag	ta	aag	gca	ac	cc	cg	cc	ag	cct	ag	cc	gg	t	ct	ca	ac	ga	cag	gag	ca	3300
ccc	gt	gg	cca	gg	ac	cca	ac	g	ct	g	cc	cg	aga	t	ct	g	at	ccc	gc	gaa	3360
tat	agg	gaga	cc	aca	ac	gg	t	tt	cc	ct	ct	ag	aa	ata	at	ttt	gt	tt	a	act	3420
tata	cat	atg	ccc	aac	agt	gag	ccc	gca	tct	ctg	ctg	gag	ctg	ttc	aac						3469
		Met	Pro	Asn	Ser	Glu	Pro	Ala	Ser	Leu	Leu	Glu	Leu	Phe	Asn						
		1				5					10										
agc	atc	gcc	aca	caa	ggg	gag	ctc	gta	agg	tcc	ctc	aaa	gcg	gga	aat						3517
Ser	Ile	Ala	Thr	Gln	Gly	Glu	Leu	Val	Arg	Ser	Leu	Lys	Ala	Gly	Asn						
	15				20				25						30						
gcg	tca	aag	gat	gaa	att	gat	tct	gca	gta	aag	atg	ttg	gtg	tca	tta						3565
Ala	Ser	Lys	Asp	Glu	Ile	Asp	Ser	Ala	Val	Lys	Met	Leu	Val	Ser	Leu						
				35				40					45								
aaa	atg	agc	tac	aaa	gct	gcc	gcg	ggg	gag	gat	tac	aag	gct	gac	tgt						3613
Lys	Met	Ser	Tyr	Lys	Ala	Ala	Ala	Gly	Glu	Asp	Tyr	Lys	Ala	Asp	Cys						
			50					55					60								
cct	cca	ggg	aac	cca	gca	cct	acc	agt	aat	cat	ggc	cca	gat	gcc	aca						3661
Pro	Pro	Gly	Asn	Pro	Ala	Pro	Thr	Ser	Asn	His	Gly	Pro	Asp	Ala	Thr						
		65					70					75									
gaa	gct	gaa	gag	gat	ttt	gtg	gac	cca	tgg	aca	gta	cag	aca	agc	agt						3709
Glu	Ala	Glu	Glu	Asp	Phe	Val	Asp	Pro	Trp	Thr	Val	Gln	Thr	Ser	Ser						
		80				85					90										
gca	aaa	ggc	ata	gac	tac	gat</															

atg aat cag gtt ctt gat gcc tat gaa aat aag aag cca ttt tat ctg Met Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr Leu 145 150 155	3901
tac acg ggc cgg ggc ccc tct tct gaa gca atg cat gta ggt cac ctc Tyr Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His Leu 160 165 170	3949
att cca ttt att ttc aca aag tgg ctc cag gat gta ttt aac gtg ccc Ile Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val Pro 175 180 185 190	3997
ttg gtc atc cag atg acg gat gac gag aag tat ctg tgg aag gac ctg Leu Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp Leu 195 200 205	4045
acc ctg gac cag gcc tat ggc gat gct gtt gag aat gcc aag gac atc Thr Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp Ile 210 215 220	4093
atc gcc tgt ggc ttt gac atc aac aag act ttc ata ttc tct gac ctg Ile Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp Leu 225 230 235	4141
gac tac atg ggg atg agc tca ggt ttc tac aaa aat gtg gtg aag att Asp Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val Lys Ile 240 245 250	4189
caa aag cat gtt acc ttc aac caa gtg aaa ggc att ttc ggc ttc act Gln Lys His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly Phe Thr 255 260 265 270	4237
gac agc gac tgc att ggg aag atc agt ttt cct gcc atc cag gct gct Asp Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala Ala 275 280 285	4285
ccc tcc ttc agc aac tca ttc cca cag atc ttc cga gac agg acg gat Pro Ser Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr Asp 290 295 300	4333
atc cag tgc ctt atc cca tgt gcc att gac cag gat cct tac ttt aga Ile Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg 305 310 315	4381
atg aca agg gac gtc gcc ccc agg atc ggc tat cct aaa cca gcc ctg Met Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala Leu 320 325 330	4429
ttg cac tcc acc ttc ttc cca gcc ctg cag ggc gcc cag acc aaa atg Leu His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys Met 335 340 345 350	4477
agt gcc agc gac cca aac tcc tcc atc ttc ctc acc gac acg gcc aag Ser Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala Lys 355 360 365	4525
cag atc aaa acc aag gtc aat aag cat gcg ttt tct gga ggg aga gac Gln Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg Asp 370 375 380	4573



acc atc gag gag cac agg cag ttt ggg ggc aac tgt gat gtg gac gtg 4621  
 Thr Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val Asp Val  
 385 390 395

tct ttc atg tac ctg acc ttc ttc ctc gag gac gac gac aag ctc gag 4669  
 Ser Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu Glu  
 400 405 410

cag atc agg aag gat tac acc agc gga gcc atg ctc acc ggt gag ctc 4717  
 Gln Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu Leu  
 415 420 425 430

aag aag gca ctc ata gag gtt ctg cag ccc ttg atc gca gag cac cag 4765  
 Lys Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His Gln  
 435 440 445

gcc cgg cgc aag gag gtc acg gat gag ata gtg aaa gag ttc atg act 4813  
 Ala Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met Thr  
 450 455 460

ccc cgg aag ctg tcc ttc gac ttt cag aag ctt gcg gcc gca ctc gag 4861  
 Pro Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala Ala Ala Leu Glu  
 465 470 475

cac cac cac cac cac cac tgagatccgg ctgctaacaa agcccgaag 4909  
 His His His His His His  
 480

gaagctgagt tggctgctgc caccgctgag caataactag cataaccct tggggcctct 4969  
 aaacgggtct tgaggggttt ttgctgaaa ggaggaacta tatccggat 5018

<210> 10  
 <211> 484  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: human  
 full-length TrpRS in pET20B

<400> 10  
 Met Pro Asn Ser Glu Pro Ala Ser Leu Leu Glu Leu Phe Asn Ser Ile  
 1 5 10 15  
 Ala Thr Gln Gly Glu Leu Val Arg Ser Leu Lys Ala Gly Asn Ala Ser  
 20 25 30  
 Lys Asp Glu Ile Asp Ser Ala Val Lys Met Leu Val Ser Leu Lys Met  
 35 40 45  
 Ser Tyr Lys Ala Ala Ala Gly Glu Asp Tyr Lys Ala Asp Cys Pro Pro  
 50 55 60  
 Gly Asn Pro Ala Pro Thr Ser Asn His Gly Pro Asp Ala Thr Glu Ala  
 65 70 75 80  
 Glu Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys  
 85 90 95

Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys Ile  
 100 105 110  
 Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg Pro  
 115 120 125  
 His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His Arg Asp Met Asn  
 130 135 140  
 Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr Leu Tyr Thr  
 145 150 155 160  
 Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His Leu Ile Pro  
 165 170 175  
 Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val Pro Leu Val  
 180 185 190  
 Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp Leu Thr Leu  
 195 200 205  
 Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp Ile Ile Ala  
 210 215 220  
 Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp Tyr  
 225 230 235 240  
 Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val Lys Ile Gln Lys  
 245 250 255  
 His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly Phe Thr Asp Ser  
 260 265 270  
 Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro Ser  
 275 280 285  
 Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile Gln  
 290 295 300  
 Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr  
 305 310 315 320  
 Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu His  
 325 330 335  
 Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys Met Ser Ala  
 340 345 350  
 Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln Ile  
 355 360 365  
 Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg Asp Thr Ile  
 370 375 380  
 Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val Asp Val Ser Phe  
 385 390 395 400  
 Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu Glu Gln Ile  
 405 410 415  
 Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu Leu Lys Lys  
 420 425 430

Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His Gln Ala Arg  
 435 440 445

Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met Thr Pro Arg  
 450 455 460

Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala Ala Ala Leu Glu His His  
 465 470 475 480

His His His His

<210> 11  
 <211> 4877  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (3428)..(4738)

<220>  
 <223> Description of Artificial Sequence: human mini  
 TrpRS in pET20B

<400> 11  
 tggcgaatgg gacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg tggttacgcg 60  
 cagcgtgacc gctacacttg ccagcgccct agcgcccgct cctttcgctt tcttcccttc 120  
 ctttctcgcc acgttcgcgc gctttcccg tcaagctcta aatcgggggc tccctttagg 180  
 gttccgattt agtgctttac ggcacctoga ccccaaaaaa cttgattagg gtgatgggtc 240  
 acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtcc'acgtt 300  
 ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggctctattc 360  
 ttttgattta taagggattt tgccgatttc ggccatttgg ttaaaaaatg agctgattta 420  
 acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt 480  
 tcgggggaaat gtgcgcggaa cccctatttg tttatttttc taaatacatt caaatatgta 540  
 tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa ggaagagtat 600  
 gagtattcaa catttccgtg tcgcccttat tccctttttt gcggcatttt gccttctctgt 660  
 ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg 720  
 agtgggttac atogaactgg atctcaacag cggtaaagatc cttgagagtt ttcgccccga 780  
 agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcggt tattatcccg 840  
 tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga atgacttgggt 900  
 tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa gagaattatg 960  
 cagtgtctgcc ataaccatga gtgataacac tgcggcccaac ttactttctga caacgatcgg 1020

aggaccgaag gagctaaccg cttttttgca caacatgggg gatcatgtaa ctgcgcttga 1080  
tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca ccacgatgcc 1140  
tgcagcaatg gcaacaacgt tgcgcaaact attaactggc gaactactta ctctagcttc 1200  
ccggcaacaa ttaatagact ggatggaggg ggataaagtt gcaggaccac ttctgcgctc 1260  
ggcccttccg gctggctggg ttattgctga taaatctgga gccggtgagc gtgggtctcg 1320  
cggtatcatt gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac 1380  
gacggggagt caggcaacta tggatgaacg aaatagacag atcgctgaga taggtgcctc 1440  
actgattaag cattggtaac tgtcagacca agtttactca tatatacttt agattgattt 1500  
aaaacttcat ttttaattta aaaggatcta ggtgaagatc ctttttgata atctcatgac 1560  
caaaatccct taacgtgagt tttcgttcca ctgagcgtca gaccccgtag aaaagatcaa 1620  
aggatcttct tgagatcctt ttttctgcyg cgtaatctgc tgcttgcaaa caaaaaaac 1680  
accgctacca gcggtgggtt gtttgccgga tcaagagcta ccaactcttt ttccgaagg 1740  
aactggcttc agcagagcgc agataccaaa tactgtcctt ctagtgtagc cgtagttagg 1800  
ccaccacttc aagaactctg tagcaccgcc tacatactc gctctgctaa tctgttacc 1860  
agtggctgct gccagtggcg ataagtcgtg tcttaccggg ttggactcaa gacgatagtt 1920  
accggataag gcgcagcggg cgggctgaac ggggggttcg tgcacacagc ccagcttgga 1980  
gcgaacgacc tacaccgaac tgagatacct acagcgtgag ctatgagaaa gcgccacgct 2040  
tcccgaaggg agaaaggcgg acaggatatc ggtaagcggc agggtcggaa caggagagcg 2100  
cacgagggag cttccagggg gaaacgcctg gtatctttat agtcctgtcg ggtttcgcca 2160  
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cgccagcaac gcggcctttt tacggttcct ggcccttttg tggccttttg ctacatggt 2280  
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 tatacat atg agc tac aaa gct gcc gcg ggg gag gat tac aag gct gac 3469  
           Met Ser Tyr Lys Ala Ala Ala Gly Glu Asp Tyr Lys Ala Asp  
           1                          5                          10  
 tgt cct cca ggg aac cca gca cct acc agt aat cat ggc cca gat gcc 3517  
 Cys Pro Pro Gly Asn Pro Ala Pro Thr Ser Asn His Gly Pro Asp Ala  
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 aca gaa got gaa gag gat ttt gtg gac cca tgg aca gta cag aca agc 3565  
 Thr Glu Ala Glu Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser  
                           35                          40                          45  
 agt gca aaa ggc ata gac tac gat aag ctc att gtt cgg ttt gga agt 3613  
 Ser Ala Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser  
                           50                          55                          60  
 agt aaa att gac aaa gag cta ata aac cga ata gag aga gcc acc ggc 3661  
 Ser Lys Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly  
                           65                          70                          75  
 caa aga cca cac cac ttc ctg cgc aga ggc atc ttc ttc tca cac aga 3709  
 Gln Arg Pro His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His Arg  
       80                          85                          90  
 gat atg aat cag gtt ctt gat gcc tat gaa aat aag aag cca ttt tat 3757  
 Asp Met Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr  
       95                          100                          105                          110  
 ctg tac acg ggc cgg ggc ccc tct tct gaa gca atg cat gta ggt cac 3805  
 Leu Tyr Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His  
                           115                          120                          125  
 ctc att cca ttt att ttc aca aag tgg ctc cag gat gta ttt aac gtg 3853  
 Leu Ile Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val  
                           130                          135                          140  
 ccc ttg gtc atc cag atg acg gat gac gag aag tat ctg tgg aag gac 3901  
 Pro Leu Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp  
                           145                          150                          155  
 ctg acc ctg gac cag gcc tat ggc gat gct gtt gag aat gcc aag gac 3949  
 Leu Thr Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp  
       160                          165                          170

atc Ile 175	atc Ile	gcc Ala	tgt Cys	ggc Gly	ttt Phe 180	gac Asp	atc Ile	aac Asn	aag Lys	act Thr 185	ttc Phe	ata Ile	ttc Phe	tct Ser	gac Asp 190	3997
ctg Leu	gac Asp	tac Tyr	atg Met	ggg Gly 195	atg Met	agc Ser	tca Ser	ggt Gly	ttc Phe 200	tac Tyr	aaa Lys	aat Asn	gtg Val	gtg Val 205	aag Lys	4045
att Ile	caa Gln	aag Lys	cat His 210	gtt Val	acc Thr	ttc Phe	aac Asn	caa Gln 215	gtg Val	aaa Lys	ggc Gly	att Ile	ttc Phe 220	ggc Gly	ttc Phe	4093
act Thr	gac Asp	agc Ser 225	gac Asp	tgc Cys	att Ile	ggg Gly	aag Lys 230	atc Ile	agt Ser	ttt Phe	cct Pro	gcc Ala 235	atc Ile	cag Gln	gct Ala	4141
gct Ala	ccc Pro 240	tcc Ser	ttc Phe	agc Ser	aac Asn	tca Ser 245	ttc Phe	cca Pro	cag Gln	atc Ile	ttc Phe 250	cga Arg	gac Asp	agg Arg	acg Thr	4189
gat Asp 255	atc Ile	cag Gln	tgc Cys	ctt Leu	atc Ile 260	cca Pro	tgt Cys	gcc Ala	att Ile	gac Asp 265	cag Gln	gat Asp	cct Pro	tac Tyr	ttt Phe 270	4237
aga Arg	atg Met	aca Thr	agg Arg	gac Asp 275	gtc Val	gcc Ala	ccc Pro	agg Arg	atc Ile 280	ggc Gly	tat Tyr	cct Pro	aaa Lys	cca Pro 285	gcc Ala	4285
ctg Leu	ttg Leu	cac His	tcc Ser 290	acc Thr	ttc Phe	ttc Phe	cca Pro	gcc Ala 295	ctg Leu	cag Gln	ggc Gly	gcc Ala	cag Gln 300	acc Thr	aaa Lys	4333
atg Met	agt Ser	gcc Ala 305	agc Ser	gac Asp	cca Pro	aac Asn	tcc Ser 310	tcc Ser	atc Ile	ttc Phe	ctc Leu	acc Thr 315	gac Asp	acg Thr	gcc Ala	4381
aag Lys	cag Gln 320	atc Ile	aaa Lys	acc Thr	aag Lys	gtc Val 325	aat Asn	aag Lys	cat His	gcg Ala	ttt Phe 330	tct Ser	gga Gly	ggg Gly	aga Arg	4429
gac Asp 335	acc Thr	atc Ile	gag Glu	gag Glu	cac His 340	agg Arg	cag Gln	ttt Phe	ggg Gly	ggc Gly 345	aac Asn	tgt Cys	gat Asp	gtg Val	gac Asp 350	4477
gtg Val	tct Ser	ttc Phe	atg Met	tac Tyr 355	ctg Leu	acc Thr	ttc Phe	ttc Phe	ctc Leu 360	gag Glu	gac Asp	gac Asp	gac Asp	aag Lys 365	ctc Leu	4525
gag Glu	cag Gln	atc Ile	agg Arg	aag Lys	gat Asp	tac Tyr	acc Thr	agc Ser 375	gga Gly	gcc Ala	atg Met	ctc Leu	acc Thr 380	ggg Gly	gag Glu	4573
ctc Leu	aag Lys	aag Lys	gca Ala	ctc Leu	ata Ile	gag Glu	gtt Val 390	ctg Leu	cag Gln	ccc Pro	ttg Leu	atc Ile 395	gca Ala	gag Glu	cac His	4621
cag Gln 400	gcc Ala	cgg Arg	cgc Arg	aag Lys	gag Glu	gtc Val	acg Thr	gat Asp	gag Glu	ata Ile 410	gtg Val	aaa Lys	gag Glu	ttc Phe	atg Met	4669

act ccc cgg aag ctg tcc ttc gac ttt cag aag ctt gcg gcc gca ctc 4717  
 Thr Pro Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala Ala Ala Leu  
 415 420 425 430

gag cac cac cac cac cac cac tgagatccgg ctgctaacaa agcccgaag 4768  
 Glu His His His His His His  
 435

gaagctgagt tggctgctgc caccgctgag caataactag cataaccct tggggcctct 4828

aaacgggtct tgaggggttt tttgctgaaa ggaggaacta tatccggat 4877

<210> 12

<211> 437

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: human mini  
 TrpRS in pET20B

<400> 12

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Pro Gly Asn Pro Ala Pro Thr Ser Asn His Gly Pro Asp Ala Thr Glu  
 20 25 30

Ala Glu Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala  
 35 40 45

Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys  
 50 55 60

Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg  
 65 70 75 80

Pro His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His Arg Asp Met  
 85 90 95

Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr Leu Tyr  
 100 105 110

Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His Leu Ile  
 115 120 125

Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val Pro Leu  
 130 135 140

Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp Leu Thr  
 145 150 155 160

Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp Ile Ile  
 165 170 175

Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp  
 180 185 190

Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val Lys Ile Gln  
 195 200 205

Lys His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly Phe Thr Asp  
 210 215 220  
 Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro  
 225 230 235 240  
 Ser Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile  
 245 250 255  
 Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met  
 260 265 270  
 Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu  
 275 280 285  
 His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys Met Ser  
 290 295 300  
 Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln  
 305 310 315 320  
 Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg Asp Thr  
 325 330 335  
 Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val Asp Val Ser  
 340 345 350  
 Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu Glu Gln  
 355 360 365  
 Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu Leu Lys  
 370 375 380  
 Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His Gln Ala  
 385 390 395 400  
 Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met Thr Pro  
 405 410 415  
 Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala Ala Ala Leu Glu His  
 420 425 430  
 His His His His His  
 435

<210> 13  
 <211> 4811  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (3428)..(4672)

<220>  
 <223> Description of Artificial Sequence: human  
 supermini TrpRS in pET20B

<400> 13  
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ctttctcgcc acgttcgccc gctttccccg tcaagctcta aatcgggggc tccctttagg 180  
gttccgattt agtgctttac ggcacctoga ccccaaaaaa cttgattagg gtgatgggtc 240  
acgtagtggg ccacgcacct gatagacggt ttttcgcctt ttgacgttgg agtccacgtt 300  
ctttaatagt ggactcttgt tccaaactgg aacaacactc aacctatct cggtctattc 360  
ttttgattta taagggattt tgccgatttc ggcctattgg ttaaaaaatg agctgattta 420  
acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt 480  
tcgggggaaat gtgcgcggaa cccctatttg tttatttttc taaatacatt caaatatgta 540  
tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa ggaagagtat 600  
gagtattcaa catttccttg tcgcccttat tccctttttt gcggcatttt gccttcctgt 660  
ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg 720  
agtgggttac atcgaaactgg atctcaacag cggtaagatc cttgagagtt ttcgccccga 780  
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tattgacgcc gggcaagagc aactcggctg ccgcatacac tattctcaga atgacttgggt 900  
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accggataag gcgcagcggg cgggctgaac ggggggttcg tgcacacagc ccagcttgga 1980  
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 aaatcactca gggatcaatgc cagcgttcg ttaatacaga tgtaggtgtt ccacagggta 3060  
 gccagcagca tcctgcgatg cagatccgga acataatggg gcagggcgct gacttccgcg 3120  
 tttccagact ttacgaaaca cgaaaccga agaccattca tgttggtgct caggtcgcag 3180  
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 cagtaaggca accccgccag cctagccggg tcctcaacga caggagcacg atcatgcgca 3300  
 cccgtggcca ggaccaacg ctgcccgaga tctcgatccc gcgaaattaa tacgactcac 3360  
 tatagggaga ccacaacggt ttccctctag aaataatttt gtttaacttt aagaaggaga 3420  
 tatacat atg agt aat cat ggc cca gat gcc aca gaa gct gaa gag gat 3469  
           Met Ser Asn His Gly Pro Asp Ala Thr Glu Ala Glu Glu Asp  
           1                  5                  10  
 ttt gtg gac cca tgg aca gta cag aca agc agt gca aaa ggc ata gac 3517  
 Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys Gly Ile Asp  
       15                  20                  25                  30  
 tac gat aag ctc att gtt cgg ttt gga agt agt aaa att gac aaa gag 3565  
 Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys Ile Asp Lys Glu  
                   35                  40                  45

cta ata aac cga ata gag aga gcc acc ggc caa aga cca cac cac ttc	3613
Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg Pro His His Phe	
50 55 60	
ctg cgc aga ggc atc ttc ttc tca cac aga gat atg aat cag gtt ctt	3661
Leu Arg Arg Gly Ile Phe Phe Ser His Arg Asp Met Asn Gln Val Leu	
65 70 75	
gat gcc tat gaa aat aag aag cca ttt tat ctg tac acg ggc cgg ggc	3709
Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr Leu Tyr Thr Gly Arg Gly	
80 85 90	
ccc tct tct gaa gca atg cat gta ggt cac ctc att cca ttt att ttc	3757
Pro Ser Ser Glu Ala Met His Val Gly His Leu Ile Pro Phe Ile Phe	
95 100 105 110	
aca aag tgg ctc cag gat gta ttt aac gtg ccc ttg gtc atc cag atg	3805
Thr Lys Trp Leu Gln Asp Val Phe Asn Val Pro Leu Val Ile Gln Met	
115 120 125	
acg gat gac gag aag tat ctg tgg aag gac ctg acc ctg gac cag gcc	3853
Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp Leu Thr Leu Asp Gln Ala	
130 135 140	
tat ggc gat gct gtt gag aat gcc aag gac atc atc gcc tgt ggc ttt	3901
Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp Ile Ile Ala Cys Gly Phe	
145 150 155	
gac atc aac aag act ttc ata ttc tct gac ctg gac tac atg ggg atg	3949
Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp Tyr Met Gly Met	
160 165 170	
agc tca ggt ttc tac aaa aat gtg gtg aag att caa aag cat gtt acc	3997
Ser Ser Gly Phe Tyr Lys Asn Val Val Lys Ile Gln Lys His Val Thr	
175 180 185 190	
ttc aac caa gtg aaa ggc att ttc ggc ttc act gac agc gac tgc att	4045
Phe Asn Gln Val Lys Gly Ile Phe Gly Phe Thr Asp Ser Asp Cys Ile	
195 200 205	
ggg aag atc agt ttt cct gcc atc cag gct gct ccc tcc ttc agc aac	4093
Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro Ser Phe Ser Asn	
210 215 220	
tca ttc cca cag atc ttc cga gac agg acg gat atc cag tgc ctt atc	4141
Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile Gln Cys Leu Ile	
225 230 235	
cca tgt gcc att gac cag gat cct tac ttt aga atg aca agg gac gtc	4189
Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr Arg Asp Val	
240 245 250	
gcc ccc agg atc ggc tat cct aaa cca gcc ctg ttg cac tcc acc ttc	4237
Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu His Ser Thr Phe	
255 260 265 270	
ttc cca gcc ctg cag ggc gcc cag acc aaa atg agt gcc agc gac cca	4285
Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys Met Ser Ala Ser Asp Pro	
275 280 285	

aac tcc tcc atc ttc ctc acc gac acg gcc aag cag atc aaa acc aag 4333  
 Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln Ile Lys Thr Lys  
 290 295 300

gtc aat aag cat gcg ttt tct gga ggg aga gac acc atc gag gag cac 4381  
 Val Asn Lys His Ala Phe Ser Gly Gly Arg Asp Thr Ile Glu Glu His  
 305 310 315

agg cag ttt ggg ggc aac tgt gat gtg gac gtg tct ttc atg tac ctg 4429  
 Arg Gln Phe Gly Gly Asn Cys Asp Val Asp Val Ser Phe Met Tyr Leu  
 320 325 330

acc ttc ttc ctc gag gac gac gac aag ctc gag cag atc agg aag gat 4477  
 Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu Glu Gln Ile Arg Lys Asp  
 335 340 345 350

tac acc agc gga gcc atg ctc acc ggt gag ctc aag aag gca ctc ata 4525  
 Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu Leu Lys Lys Ala Leu Ile  
 355 360 365

gag gtt ctg cag ccc ttg atc gca gag cac cag gcc cgg cgc aag gag 4573  
 Glu Val Leu Gln Pro Leu Ile Ala Glu His Gln Ala Arg Arg Lys Glu  
 370 375 380

gtc acg gat gag ata gtg aaa gag ttc atg act ccc cgg aag ctg tcc 4621  
 Val Thr Asp Glu Ile Val Lys Glu Phe Met Thr Pro Arg Lys Leu Ser  
 385 390 395

ttc gac ttt cag aag ctt gcg gcc gca ctc gag cac cac cac cac cac 4669  
 Phe Asp Phe Gln Lys Leu Ala Ala Leu Glu His His His His His  
 400 405 410

cac tgagatccgg ctgctaacaa agcccgaaag gaagctgagt tggctgctgc 4722  
 His  
 415

caccgctgag caataactag cataaccct tggggcctct aaacgggtct tgagggggttt 4782

tttgctgaaa ggaggaacta tatccggat 4811

&lt;210&gt; 14

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence: human  
 supermini TrpRS in pET20B

&lt;400&gt; 14

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 1 5 10 15

 Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys Gly Ile Asp Tyr Asp  
 20 25 30

 Lys Leu Ile Val Arg Phe Gly Ser Ser Lys Ile Asp Lys Glu Leu Ile  
 35 40 45

 Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg Pro His His Phe Leu Arg  
 50 55 60

Arg Gly Ile Phe Phe Ser His Arg Asp Met Asn Gln Val Leu Asp Ala  
 65 70 75 80  
 Tyr Glu Asn Lys Lys Pro Phe Tyr Leu Tyr Thr Gly Arg Gly Pro Ser  
 85 90 95  
 Ser Glu Ala Met His Val Gly His Leu Ile Pro Phe Ile Phe Thr Lys  
 100 105 110  
 Trp Leu Gln Asp Val Phe Asn Val Pro Leu Val Ile Gln Met Thr Asp  
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 Asp Glu Lys Tyr Leu Trp Lys Asp Leu Thr Leu Asp Gln Ala Tyr Gly  
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 Asp Ala Val Glu Asn Ala Lys Asp Ile Ile Ala Cys Gly Phe Asp Ile  
 145 150 155 160  
 Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp Tyr Met Gly Met Ser Ser  
 165 170 175  
 Gly Phe Tyr Lys Asn Val Val Lys Ile Gln Lys His Val Thr Phe Asn  
 180 185 190  
 Gln Val Lys Gly Ile Phe Gly Phe Thr Asp Ser Asp Cys Ile Gly Lys  
 195 200 205  
 Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro Ser Phe Ser Asn Ser Phe  
 210 215 220  
 Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile Gln Cys Leu Ile Pro Cys  
 225 230 235 240  
 Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr Arg Asp Val Ala Pro  
 245 250 255  
 Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu His Ser Thr Phe Phe Pro  
 260 265 270  
 Ala Leu Gln Gly Ala Gln Thr Lys Met Ser Ala Ser Asp Pro Asn Ser  
 275 280 285  
 Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln Ile Lys Thr Lys Val Asn  
 290 295 300  
 Lys His Ala Phe Ser Gly Gly Arg Asp Thr Ile Glu Glu His Arg Gln  
 305 310 315 320  
 Phe Gly Gly Asn Cys Asp Val Asp Val Ser Phe Met Tyr Leu Thr Phe  
 325 330 335  
 Phe Leu Glu Asp Asp Asp Lys Leu Glu Gln Ile Arg Lys Asp Tyr Thr  
 340 345 350  
 Ser Gly Ala Met Leu Thr Gly Glu Leu Lys Lys Ala Leu Ile Glu Val  
 355 360 365  
 Leu Gln Pro Leu Ile Ala Glu His Gln Ala Arg Arg Lys Glu Val Thr  
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Asp Glu Ile Val Lys Glu Phe Met Thr Pro Arg Lys Leu Ser Phe Asp  
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<211> 4742

<212> DNA

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<222> (3428)..(4603)

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<223> Description of Artificial Sequence: human minor  
 Trp-RS fragment in pET20B

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 acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacggt 300  
 ctttaatatg ggactcttgt tccaaactgg aacaacactc aaccctatct cgggtctattc 360  
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 agaacgtttt ccaatgatga gcaactttta agttctgcta tgtggcgcgg tattatcccg 840  
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 cagtgtgcc ataaccatga gtgataacac tgcggccaac ttacttctga caacgatcgg 1020  
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cagtaaggca accccgccag cctagccggg tcttcaacga caggagcacg atcatgcgca															3300
cccgtaggcca ggacccaacg ctgcccgcga tctcgatccc gcgaaattaa tacgactcac															3360
tatagggaga ccacaacggt ttccctctag aaataatttt gtttaacttt aagaaggaga															3420
tatacat atg agt gca aaa ggc ata gac tac gat aag ctc att gtt cgg															3469
Met Ser Ala Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg															
1 5 10															
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Phe Gly Ser Ser Lys Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg															
15 20 25 30															
gcc acc ggc caa aga cca cac cac ttc ctg cgc aga ggc atc ttc ttc															3565
Ala Thr Gly Gln Arg Pro His His Phe Leu Arg Arg Gly Ile Phe Phe															
35 40 45															
tca cac aga gat atg aat cag gtt ctt gat gcc tat gaa aat aag aag															3613
Ser His Arg Asp Met Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys															
50 55 60															
cca ttt tat ctg tac acg ggc cgg ggc ccc tct tct gaa gca atg cat															3661
Pro Phe Tyr Leu Tyr Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His															
65 70 75															
gta ggt cac ctc att cca ttt att ttc aca aag tgg ctc cag gat gta															3709
Val Gly His Leu Ile Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val															
80 85 90															
ttt aac gtg ccc ttg gtc atc cag atg acg gat gac gag aag tat ctg															3757
Phe Asn Val Pro Leu Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu															
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tgg aag gac ctg acc ctg gac cag gcc tat ggc gat gct gtt gag aat															3805
Trp Lys Asp Leu Thr Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn															
115 120 125															
gcc aag gac atc atc gcc tgt ggc ttt gac atc aac aag act ttc ata															3853
Ala Lys Asp Ile Ile Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile															
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ttc tct gac ctg gac tac atg ggg atg agc tca ggt ttc tac aaa aat															3901
Phe Ser Asp Leu Asp Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn															
145 150 155															
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Val Val Lys Ile Gln Lys His Val Thr Phe Asn Gln Val Lys Gly Ile															
160 165 170															
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Phe Gly Phe Thr Asp Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala															
175 180 185 190															



atc cag gct gct ccc tcc ttc agc aac tca ttc cca cag atc ttc cga 4045  
 Ile Gln Ala Ala Pro Ser Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg  
 195 200 205

gac agg acg gat atc cag tgc ctt atc cca tgt gcc att gac cag gat 4093  
 Asp Arg Thr Asp Ile Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp  
 210 215 220

cct tac ttt aga atg aca agg gac gtc gcc ccc agg atc ggc tat cct 4141  
 Pro Tyr Phe Arg Met Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro  
 225 230 235

aaa cca gcc ctg ttg cac tcc acc ttc ttc cca gcc ctg cag ggc gcc 4189  
 Lys Pro Ala Leu Leu His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala  
 240 245 250

cag acc aaa atg agt gcc agc gac cca aac tcc tcc atc ttc ctc acc 4237  
 Gln Thr Lys Met Ser Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr  
 255 260 265 270

gac acg gcc aag cag atc aaa acc aag gtc aat aag cat gcg ttt tct 4285  
 Asp Thr Ala Lys Gln Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser  
 275 280 285

gga ggg aga gac acc atc gag gag cac agg cag ttt ggg ggc aac tgt 4333  
 Gly Gly Arg Asp Thr Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys  
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gat gtg gac gtg tct ttc atg tac ctg acc ttc ttc ctc gag gac gac 4381  
 Asp Val Asp Val Ser Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp  
 305 310 315

gac aag ctc gag cag atc agg aag gat tac acc agc gga gcc atg ctc 4429  
 Asp Lys Leu Glu Gln Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu  
 320 325 330

acc ggt gag ctc aag aag gca ctc ata gag gtt ctg cag ccc ttg atc 4477  
 Thr Gly Glu Leu Lys Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile  
 335 340 345 350

gca gag cac cag gcc cgg cgc aag gag gtc acg gat gag ata gtg aaa 4525  
 Ala Glu His Gln Ala Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys  
 355 360 365

gag ttc atg act ccc cgg aag ctg tcc ttc gac ttt cag aag ctt gcg 4573  
 Glu Phe Met Thr Pro Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala  
 370 375 380

gcc gca ctc gag cac cac cac cac cac tgagatccgg ctgctaacaa 4623  
 Ala Ala Leu Glu His His His His His His  
 385 390

agcccgaag gaagctgagt tggctgctgc caccgctgag caataactag cataaccct 4683

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 TrpRS fragment in pET20B

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 Gly Gln Arg Pro His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His  
           35                  40                  45  
 Arg Asp Met Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe  
           50                  55                  60  
 Tyr Leu Tyr Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly  
           65                  70                  75                  80  
 His Leu Ile Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn  
                   85                  90                  95  
 Val Pro Leu Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys  
           100                  105                  110  
 Asp Leu Thr Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys  
           115                  120                  125  
 Asp Ile Ile Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser  
           130                  135                  140  
 Asp Leu Asp Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val  
           145                  150                  155                  160  
 Lys Ile Gln Lys His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly  
           165                  170                  175  
 Phe Thr Asp Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln  
           180                  185                  190  
 Ala Ala Pro Ser Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg  
           195                  200                  205  
 Thr Asp Ile Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr  
           210                  215                  220  
 Phe Arg Met Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro  
           225                  230                  235                  240  
 Ala Leu Leu His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr  
           245                  250                  255  
 Lys Met Ser Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr  
           260                  265                  270

Ala Lys Gln Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly  
 275 280 285

Arg Asp Thr Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val  
 290 295 300

Asp Val Ser Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys  
 305 310 315 320

Leu Glu Gln Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly  
 325 330 335

Glu Leu Lys Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu  
 340 345 350

His Gln Ala Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe  
 355 360 365

Met Thr Pro Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala Ala Ala  
 370 375 380

Leu Glu His His His His His His  
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<212> PRT

<213> Homo sapiens

<400> 17

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<212> PRT

<213> Escherichia coli

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<212> PRT

<213> Homo sapiens

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 Lys Glu Lys Lys Gln Gln Ser Ile Ala Gly Ser Ala Asp Ser Lys Pro  
                     20                    25                    30  
 Ile Asp Val Ser Arg Leu Asp Leu Arg Ile Gly Cys Ile Ile Thr Ala  
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<400> 23  
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                     20                    25                    30  
 Val Ile Pro Ser Arg Leu Asp Ile Arg Val Gly Lys Ile Ile Thr Val  
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 Glu Lys His Pro Asp Ala Asp Ser Leu Tyr  
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<400> 24  
Arg Val Gly Lys Ile Ile Thr  
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<210> 25  
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<400> 25  
Arg Ile Gly Cys Ile Ile Thr  
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<210> 26  
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<400> 26  
Arg Ile Gly Arg Ile Ile Thr  
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<210> 27  
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<210> 28  
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<400> 28  
Arg Val Gly Phe Ile Gln Lys  
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<400> 29  
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<210> 30  
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<400> 30

Arg Ile Gly Cys Ile Val Thr  
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<210> 31  
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Arg Ile Gly Arg Ile Val Thr  
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Arg Ile Gly Cys Ile Ile Thr  
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<400> 33  
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<400> 34  
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Arg Val Gly Lys Ile Val Glu  
1 5

<210> 36  
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<400> 36  
Arg Val Ala Leu Ile Glu Asn  
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<210> 38  
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 <213> Bacillus subtilis

<400> 38  
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<400> 39  
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<400> 42  
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 <213> *Synechococcus* sp.

<400> 43  
 Val Gly Arg Val Leu Glu  
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 <213> *Thermus thermophilus*

<400> 44  
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 Pro Gly Asn Pro Ala Pro Thr Ser Asn His Gly Pro Asp Ala Thr Glu  
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 Ala Glu Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala  
                   35                  40                  45  
 Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys  
   50                  55                  60  
 Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg  
   65                  70                  75                  80  
 Pro His His Phe Leu  
                   85

<210> 46  
 <211> 85  
 <212> PRT  
 <213> *Bos taurus*

<400> 46  
 Thr Ser Tyr Lys Ala Ala Thr Gly Glu Asp Tyr Lys Val Asp Cys Pro  
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 Pro Gly Asp Pro Ala Pro Glu Ser Gly Glu Gly Leu Asp Ala Thr Glu  
                   20                  25                  30  
 Ala Asp Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala  
                   35                  40                  45  
 Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys  
   50                  55                  60



Ile Asp Lys Glu Leu Val Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg  
65 70 75 80

Pro His Arg Phe Leu  
85

<210> 47

<211> 85

<212> PRT

<213> Mus musculus

<400> 47

Met Ser Tyr Lys Ala Ala Met Gly Glu Glu Tyr Lys Ala Gly Cys Pro  
1 5 10 15

Pro Gly Asn Pro Thr Ala Gly Arg Asn Cys Asp Ser Asp Ala Thr Lys  
20 25 30

Ala Ser Glu Asp Phe Val Asp Pro Trp Thr Val Arg Thr Ser Ser Ala  
35 40 45

Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Gln Pro Gly Ser Ser Lys  
50 55 60

Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg  
65 70 75 80

Pro His Arg Phe Leu  
85

<210> 48

<211> 85

<212> PRT

<213> Oryctolagus cuniculus

<400> 48

Thr Ser Tyr Lys Glu Ala Met Gly Glu Asp Tyr Lys Ala Asp Cys Pro  
1 5 10 15

Pro Gly Asn Ser Thr Pro Asp Ser His Gly Pro Asp Glu Ala Val Asp  
20 25 30

Asp Lys Glu Asp Phe Val Asp Pro Trp Thr Val Arg Thr Ser Ser Ala  
35 40 45

Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Gln Phe Gly Ser Ser Lys  
50 55 60

Ile Asp Lys Glu Leu Val Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg  
65 70 75 80

Pro His Arg Phe Leu  
85

<210> 49  
 <211> 86  
 <212> PRT  
 <213> Homo sapiens

<400> 49  
 Ile Ser Tyr Gln Gly Arg Ile Pro Tyr Pro Arg Pro Gly Thr Cys Pro  
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 Gly Gly Ala Phe Thr Pro Asn Met Arg Thr Thr Lys Glu Phe Pro Asp  
 20 25 30  
 Asp Val Val Thr Phe Ile Arg Asn His Pro Leu Met Tyr Asn Ser Ile  
 35 40 45  
 Tyr Pro Ile His Lys Arg Pro Leu Ile Val Arg Ile Gly Thr Asp Tyr  
 50 55 60  
 Lys Tyr Thr Lys Ile Ala Val Asp Arg Val Asn Ala Ala Asp Gly Arg  
 65 70 75 80  
 Tyr His Val Leu Phe Leu  
 85

<210> 50  
 <211> 86  
 <212> PRT  
 <213> Mus musculus

<400> 50  
 Ile Ser Tyr Gln Gly Arg Ile Pro Tyr Pro Arg Pro Gly Thr Cys Pro  
 1 5 10 15  
 Gly Gly Ala Phe Thr Pro Asn Met Arg Thr Thr Lys Asp Phe Pro Asp  
 20 25 30  
 Asp Val Val Thr Phe Ile Arg Asn His Pro Leu Met Tyr Asn Ser Ile  
 35 40 45  
 Ser Pro Ile His Arg Arg Pro Leu Ile Val Arg Ile Gly Thr Asp Tyr  
 50 55 60  
 Lys Tyr Thr Lys Ile Ala Val Asp Arg Val Asn Ala Ala Asp Gly Arg  
 65 70 75 80  
 Tyr His Val Leu Phe Leu  
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<210> 51  
 <211> 46  
 <212> PRT  
 <213> Homo sapiens

<400> 51  
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 Ala Pro Thr Ser Asn His Gly Pro Asp Ala Thr Glu Ala Glu Glu Asp  
 20 25 30

Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys Gly  
                   35                  40                  45

<210> 52  
 <211> 46  
 <212> PRT  
 <213> Bos taurus

<400> 52  
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Ala Pro Glu Ser Gly Glu Gly Leu Asp Ala Thr Glu Ala Asp Glu Asp  
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Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys Gly  
                   35                  40                  45

<210> 53  
 <211> 46  
 <212> PRT  
 <213> Mus musculus

<400> 53  
 Ala Ala Met Gly Glu Glu Tyr Lys Ala Gly Cys Pro Pro Gly Asn Pro  
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Thr Ala Gly Arg Asn Cys Asp Ser Asp Ala Thr Lys Ala Ser Glu Asp  
                   20                  25                  30

Phe Val Asp Pro Trp Thr Val Arg Thr Ser Ser Ala Lys Gly  
                   35                  40                  45

<210> 54  
 <211> 46  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 54  
 Glu Ala Met Gly Glu Asp Tyr Lys Ala Asp Cys Pro Pro Gly Asn Ser  
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Thr Pro Asp Ser His Gly Pro Asp Glu Ala Val Asp Asp Lys Glu Asp  
                   20                  25                  30

Phe Val Asp Pro Trp Thr Val Arg Thr Ser Ser Ala Lys Gly  
                   35                  40                  45

<210> 55  
 <211> 41  
 <212> PRT  
 <213> Mus musculus

<400> 55  
 Ala Phe Ala Gly Glu Asp Phe Lys Val Asp Ile Pro Glu Thr His Gly  
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Gly Glu Gly Thr Glu Asp Glu Ile Asp Asp Glu Tyr Glu Gly Asp Trp  
                   20                                  25                                  30

Ser Asn Ser Ser Ser Ser Thr Ser Gly  
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<210> 56  
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 <212> PRT  
 <213> Homo sapiens

<400> 56  
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<210> 57  
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 <212> PRT  
 <213> Homo sapiens

<400> 57  
 Ser Asn His Gly Pro  
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<210> 58  
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 <212> PRT  
 <213> Homo sapiens

<400> 58  
 Ser Ala Lys Gly Ile  
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